

IN THE FIGURES:

Please replace Figures 3A-B, 6, 7A-B, and 8 with the revised Figures 3A-D, 6, 7A-D, and 8 attached herewith.



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9 18 27 36 45 54
CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG CAG ATT [SEQ ID NO: 1]

L E M Q R N L G A V L G I L W V Q I [SEQ ID NO: 2]

63 72 81 90 99 108
TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC TTG GTT CTG CAG

C W L K E Q Q V Q Q S P A S L V L Q

117 126 135 144 153 162
GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC ATC TTT ACA AAC CAG GTG

E G E N A E L Q C S F S I F T N Q V

171 180 189 198 207 216
CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA CTC GTC AGC CTG TTG TAC AAT CCT

Q W F Y Q R P G G R L V S L L Y N P

225 234 243 252 261 270
TCT GGG ACA AAG CAG AGT GGG AGA CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT

S G T K Q S G R L T S T T V I K E R

279 288 297 306 315 324
CGC AGC TCT TTG CAC ATT TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC

R S S L H I S S S Q I T D S G T Y L

FIG. 3A



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333	342	351	360	369	378
TGT GCC TCA AAT TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT					

C	A	S	N	S	G
G	G	S	N	A	K
L	T	F	G	K	G
					T

387	396	405	414	423	432
AAA CTC TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT					

K	L	S	V	K	S
G	G	G	G	G	G
G	G	S	G	G	G
					G

441	450	459	468	477	486
GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA GTA ACA					

G	G	S	E	A	A
V	T	Q	S	P	R
N	K	V	A	V	T

495	504	513	522	531	540
GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC AAC AAC ATG TAC					

G	G	K	V	T	L
S	C	N	Q	T	N
H	N	H	N	N	M
N	M	Y			

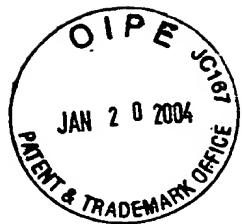
549	558	567	576	585	594
TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAT TCA TAT GGT					

W	Y	R	Q	D	T
G	H	G	L	R	L
I	H	Y	S	Y	G

603	612	621	630	639	648
GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT GAT GGA TAC AAG GCC TCC AGA CCA					

A	G	S	T	E	K
G	D	I	P	D	G
Y	K	A	S	R	P

FIG. 3B



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657	666	675	684	693	702
AGC CAA GAG AAC TTC TCC CTC ATT CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA					
<hr/>					
S	Q	E	N	F	S
L	I	L	E	L	A
T	P	S	Q	T	S
711	720	729	738	747	756
GTG TAC TTC TGT GCC AGC GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT					
<hr/>					
V	Y	F	C	A	S
G	E	T	G	T	N
R	L	F	F		G
765	774	783	792	801	810
CAT GGA ACC AAG CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC					
<hr/>					
H	G	T	K	L	S
V	L	T	S	N	S
I	M	Y	F	S	H
819	828	837	846	855	864
TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA					
<hr/>					
F	V	P	V	F	L
P	A	K	P	T	T
T	P	R	P	R	P
873	882	891	900	909	918
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA TCT AGT					
<hr/>					
P	T	P	A	P	T
I	A	S	Q	P	L
S	L	R	P	S	S
927	936	945	954	963	972
TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC ATC TAT GGT					
<hr/>					
S	R	D	P	K	L
C	Y	L	L	D	G
I	L	F	I	Y	G

FIG. 3C



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981 990 999 1008 1017 1026
GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC ACC AGG AGC GCA GAC GCC

V I L T A L F L R V K F S R S A D A

1035 1044 1053 1062 1071 1080
CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT AAC GAG GTC AAT CTA GGA CGA

P A Y Q Q G Q N Q L Y N E L N L G R

1089 1098 1107 1116 1125 1134
AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG

R E E Y D V L D K R R G R D P E M G

1143 1152 1161 1170 1179 1188
GGA AAG CCG AGA AGG AAG AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA

G K P R R K N P Q E G L Y N E L Q K

1197 1206 1215 1224 1233 1242
GAT AAG ATG GCG GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG

D K M A E A Y S E I G M K G E R R R

1251 1260 1269 1278 1287 1296
GGC AAG GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC

G K G H D G L Y Q G L S T A T K D T

1305 1314 1323 1332
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAA

Y D A L H M Q A L P P R *

FIG. 3D



Alpha Groups

											<u>SEQ ID NO.</u>
1.											
V α 1	CCC	AAG	GCA	CTG	ATG	TTC	ATC	TTC			3
V α 2	TGA	GAC	AAA	GTC	CCC	AAT	CTC	TGA	CAG		4
V α 3	CTG	CAG	CTG	CTC	CTC	AAG	TAC	TAT	TC		5
V α 4,1,2,3	TCC	CGG	AGA	AGG	TCC	ACA	GTT	CCT	CTT	T	6
V α 4,4	GAA	GCA	GCA	GAG	GGT	TTG	AAG	CCA	CAT	AC	7
2.											
V α 5	GGC	AGG	TCT	TCA	GTT	GCT	TAT	GAA	GGT		8
V α 6	GGT	TCC	TCT	TCA	GGG	TCC	AGA	ATA	TGT		9
V α 7	GCG	AAG	AAC	TCA	CCC	TGG	ACT	GTT	CAT		10
V α 8	GAG	CTC	CAC	AGA	CAA	CAA	GAG	GAC	CGA	GCA	11
V α 9	GAG	CTG	CGA	CGT	TCC	TTA	GTG	ACT	GTG		12
3.											
V α 10	CCT	CGT	CAG	CCT	GTT	GTC	CAA	TCC	TTC	TGG	13
V α 11	CAG	CCT	CAT	CAA	TCT	GTT	CTA	CTT	GGC	T	14
V α 12	CCA	CCA	GGG	ACC	ACA	GTT	TAT	CAT	TCA	A	15
V α 14	ACC	TGG	AGA	GAA	TCC	TAA	GCT	CAT	CAT		16
V α 15	AGG	TCT	TGT	GTC	CCT	GAC	AGT	CCT	GGT	T	17
4.											
V α 16	CAA	GCA	AAC	ACT	GTA	GTC	CAG	AGC	CCT	TCC	18
V α 17	CAA	GAC	ATC	CAT	AAC	TGC	CCT	ACA	G		19
V α 18	GTG	TAT	GAA	ACC	CAG	GAC	AGT	TCT	TAC		20
V α 19	CCG	TAT	TTC	TTT	CTT	ATG	TTG	TTT	TGG	AT	21
V α 20	CAA	AGC	TCT	CCA	TCG	CTG	ACT	GTT	CAA	G	22

Beta Groups

1.											
V β 1	ATC	TAA	TCC	TGG	GAA	GAG	CAA	AT			23
V β 2	GGC	GTC	TGG	TAC	CAC	GTG	GTC	AA			24
V β 3	GTG	AAA	GGG	CAA	GGA	CAA	AAA	GC			25
V β 4	GAT	ATG	CGA	ACA	GTA	TCT	AGG	C			26
V β 5,1	ACA	TAA	TCA	AAG	GAA	AGG	GAG	AA			27
2.											
V β 6	TCC	TGA	TTG	GTC	AGG	AAG	GGC	AA			28
V β 7	TAC	CTG	ATC	AAA	AGA	ATG	GGA	GA			29
V β 8,1	ATA	ACC	ATG	ACA	ATA	TGT	ACT	GG			30
V β 8,2	ATA	ACC	ACA	ACA	ACA	TGT	ACT	GG			31
V β 8,3	ATA	GCC	ACA	ACT	ACA	TGT	ACT	GG			32
3.											
V β 9	AGC	TTG	CAA	GAG	TTG	GAA	AAC	CA			33
V β 10	GAT	TAT	GTT	TAG	CTA	CAA	TAA	TA			34
V β 11	ACA	AGG	TGA	CAG	GGA	AGG	GAC	AA			35
V β 12	ACC	TAC	AGA	ACC	CAA	GGA	CTC	AG			36
V β 13	CAG	TTG	CCC	TCG	GAT	CGA	TTT	TC			37
4.											
V β 14	GCC	GAG	ATC	AAG	GCT	GTG	GGC	AG			38
V β 15	AGA	ACC	ATC	TGT	AAG	AGT	GGA	AC			39
V β 16	CAT	CAA	ATA	ATA	GAT	ATG	GGG	CA			40
V β 17	GTA	GTC	CTG	AAA	AAG	GGC	ACA	CT			41
V β 18	CAT	CTG	TCA	AAG	TGG	CAC	TTC	A			42

FIG. 6



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9	18	27	36	45	54	
ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTG TGG CTC CAG TTA AAC TGG GTG						[SEQ ID NO: 43]

Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn Trp Val						[SEQ ID NO: 44]

63	72	81	90	99	108	
CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT GTC CCA GAG GGA						

Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser Val Pro Glu Gly						

117	126	135	144	153	162	
GGC ATG GCC TCT CTC AAC TGC ACT TCA AGT GAT CGC AAT TTT CAG TAT TTC TGG						

Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg Asn Phe Gln Tyr Phe Trp						

171	180	189	198	207	216	
TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC AAA GCA CTG ATG TCC ATC TTC TCT						

Trp Tyr Arg Gln His Ser Gly Glu Gly Pro Lys Ala Leu Met Ser Ile Phe Ser						

FIG. 7A



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225 234 243 252 261 270
GAT GGT GAC AAG AAA GAA GGC AGA TTC ACA GCT CAC CTC AAT AAG GCC AGC CTG

Asp Gly Asp Lys Lys Glu Gly Arg Phe Thr Ala His Leu Asn Lys Ala Ser Leu

279 288 297 306 315 324
CAT GTT TCC CTG CAC ATC AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC

His Val Ser Leu His Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe

333 342 351 360 369 378
TGT GCA GTT ATG GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG

Cys Ala Val Met Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys

387
TTA TCT ATC AAG CCC 3'

Leu Ser Ile Lys Pro

FIG. 7B



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9	18	27	36	45	54	
ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG						[SEQ ID NO: 45]

Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys His Met						[SEQ ID NO: 46]

63	72	81	90	99	108	
GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG						

Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys						

117	126	135	144	153	162	
GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG						

Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arg						

171	180	189	198	207	216	
CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC						

Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser						

FIG. 7C



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225 234 243 252 261 270
ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG

Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu

279 288 297 306 315 324
AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC

Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe

333 342 351 360 369 378
TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT

Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly

387 396
CCC GGC ACC AGG CTC ACG GTT TCT 3'

Pro Gly Thr Arg Leu Thr Val Ser

FIG. 7D



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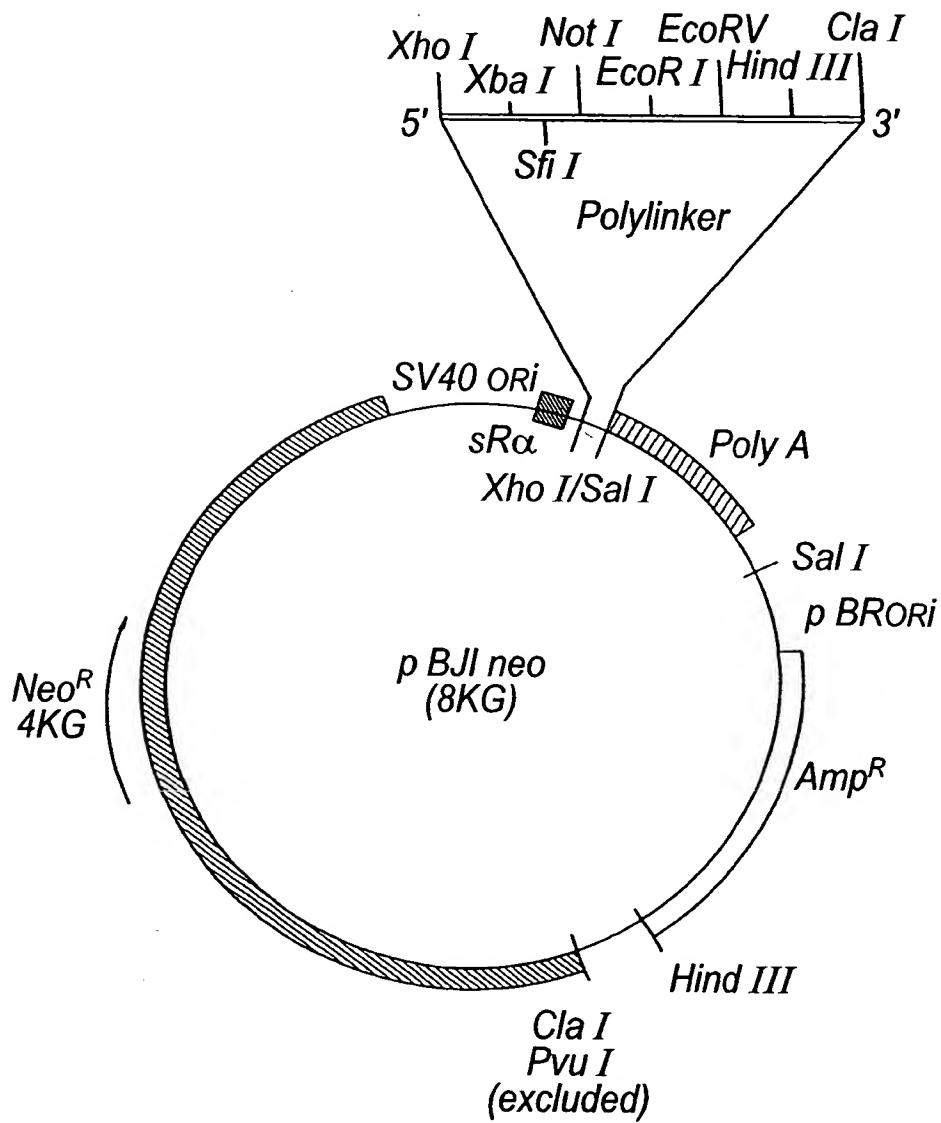


FIG. 8